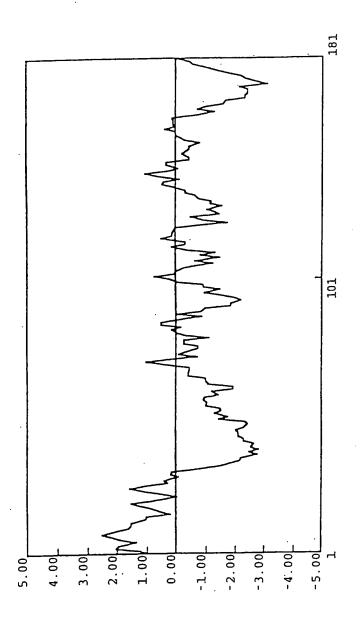
				9	n mc:	18	3 .	\	27 2 TTC	7 ייזי בי	יייי יו		6 'G AC	ጥ ጥጥ		5 C AC	יד ידכ	54 A AGC
5'						·												
	Met	Gl	u Il	e Ile	e Ser	Sei	Lys	: Le	ı Phe	e Il	e Le	u Le	u Th	r Le	u Al	a Th	r Se	r Ser
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	Leu	Lei	ı Thi	r Sei	Asn	Il∈	Phe	. Cys	: Ala	Ası	o Glu	ı Le	u Va.	1 Me	t Se	r As	n Le	u His
			117	7		126	;		135	•		14	4		15			162
	AGC	AAA	GAZ	AAT	TAT	GAC	AAA	TAT	TCT	GAC	CCI	AG	A GG	A TAC	CC	A AA	A GG	G GAA
																		7 Glu
	Ser	гЛя	i GIL	I ASII	TYL	ASP	ב עב							•			• •	
			171			180	G))	mm »	189	CAT	TCC	198	3 3	. ΔΔΔ	207 מממ		י אייים	216 AAG
	Arg	Ser	Leu	Asn	Phe	Glu	Glu	Leu	Lys	Asp	Trp	Gly	, Pro	Lys	Asn	Va]	. Ile	Lys
			225			234			243			252			261			270
	ATG	AGT	ACA	CCT	GCA	GTC	AAT	AAA	ATG	CCA	CAC	TCC	TTC	GCC	AAC	TTC	CCA	TTG
				 Dro		Val	a	Lvs	Met.	Pro	His	Ser	Phe	Ala	Asn	Leu	Pro	Leu
	Met	Ser	. 1111	PIO	ALA	467	A.J.	ביינים							•			
			279			288	~ A A	C N N	297	A C A	λсπ	306 CCT		GCA	315 ACA	GCC	· AAC	324 CTG
	Arg	Phe	Glý	Arg	Asn	Val	Gln	Glu	Glu	Arg	Ser	Ala	Gly	Ala	Thr	Ala	Asn	Leu
			333			342			351			360	•		369			378
	CCT	CTG	AGA	TCT	GGA	AGA	AAT	ATG	GAG	GTG	AGC	CTC	GTG	AGA	CGT	GTT	CCT	AAC
				Ser														
	Pro	Leu	Arg	Ser	CTÀ	AIG	ASII	Mec	Giu	· u _	-	Dou	,	,				
			387			396			405		666	414	N CM	CTC	423 TCC	N.C.C.	λTC	432 CTG
	CTG	CCC	CAA	AGG	TTT	GGG	AGA	ACA	ACA	ACA			AG1					
	Leu	Pro	Gln	Arg	Phe	Gly	Arg	Thr	Thr	Thr	Ala	Lys	Ser	Val	Cys	Arg	Met	Leu
				-			•					468			477			486
	n cm	C N TT	441	TGT	C	450 GGA	TCC	ATG	459 CAT	TCA	CCA		GCC	AAT		TTA	TTT	
	_																	
	Ser	Asp	Leu	Cys	Gln	Gly	Ser	Met	His	Ser	Pro	Cys	Ala	Asn	Asp	Leu	Phe	Tyr
			405			504			513		•	522			531			540
	TCC	эта	495 ACC	TGC	CAG	CAC	CAA	GAA	ATC	CAG	AAT	CCC	GAT	CAA	AAA	CAG	TCA	AGG
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	Ser	Met	Thr	Cys	Gln	His	Gln	Glu	Ile	Gln	Asn	Pro	Asp	GTU	гÀг	CID	ser	wed

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5'	ATG	GAA	TTA	TTA	TCA	TCA	AAA	CTA	TIC	ATT	11A							
	 Met	Glu	 Ile	Ile	Ser	Ser	Lys	Leu	Phe	Ile	Leu	Leu	Thr	Leu	Ala	Thr	Ser	Ser
									0.1	GAT		۵Ω			99			108
	TIG												 Val	~ Met	 Ser	Asn	Leu	His
	Leu	Leu	Thr	Ser	Asn	Ile	Phe	Cys	Ala	Asp	Giu		Val.	1100				162
	AGC	AAA	117 GAA	TAA	TAT	126 GAC	AAA	TAT	135 TCT	GAG	CCT	144 AGA	GGA	TAC	153 CCA	AAA 	GGG	GAA
		INS	Glu	 Asn	Tyr	Asp	Lys	Tyr	Ser	Glu	Pro	Arg	Gly	Tyr	Pro	Lys	Gly	GIu
	AGA	AGC	171 CTC	TAA	TTT	180 GAG	GAA	TTA	189 AAA	GAT	TGG	198 GGA	CCA	AAA	207 AAT	GTT	TTA	216 AAG
				 Asn	Phe	Glu	Glu	Leu	Lys	Asp	Trp	Gly	Pro	Lys	Asn	Val	Ile	Lys
									- 4 -			252			261			270
	A1G	AG1							 Mot	Pro	 His	 Ser	Phe	Ala	Asn	Leu	Pro	Leu
	Met	Ser	Thr	Pro	Ala	Val	Asn	гуs			1110				315			324
	AGA	TTT	279 GGG	AGG	AAC	GTT	CAA	GAA	297 GAA	AGA	AGT	GCT	GGA	GCA	ACA	GCC	AAC	CTG
	 Ara	Phe	Gly	Arg	Asn	Val	Gln	Glu	Glu	Arg	Ser	Ala	Gly	Ala	Thr	Ala	ASI	Leu
				•			AAT	ATG	351 GAG	GTG	AGC	360 CTC	•		369			378 AAC
							7	 Met	Glu	 Val	Ser	Leu	Val	Arg	Arg	Val	Pro	Asn
									405			111			423			432
	CTG	CCC	CAA	AGG	TTT	GGG	AGA	ACA	ACA	ACA								CTG
	 Leu	Pro	Gln	Arg	Phe	Gly	Arg	Thr	Thr	Thr	Ala	Lys	Ser	Val	Cys	Arg	Met	Leu
	AGT	GAT	441 TTG	TGT	CAA	450 GGA	TCC	ATG	459 CAT	TCA	CCA	468 TGT	GCC	AAT	477 GAC	TTA	TTT	486 TAC
							 Ser	Met	 His	Ser	Pro	Cys	Ala	Asn	Asp	Leu	Phe	Tyr
	Ser	Asp	Leu	Суѕ	GIH	. Gry									531			540
	TCC	ATG	495 ACC	TGC	CAG	504 CAC	CAA	GAA	513 ATC	CAG	AAT	522 CCC	GAT	CAA	AAA 	CAG	TCA	AGG
	Ser	Met	Thr	Cys	Gln	His	Gln	Glu	Ile	Gln	Asn	Pro	Asp	GIN	гЛs	GIN	⊃ ∈ 1.	Arg
												576			585			
	Arg	Leu	Leu	 Phe	Lys	Lys	Ile	Asp	Asp	Ala	Glu	Leu	Lys	Gln	Glu	Lys	***	

	ATG		9	አጥጥ	αΥn	18 TTA	AÀA	CGA	27 TTC	TTA	TTA	36 TTG	ATG	TTA	45 GCC	ACT	TCA	54 AGC
5 '	ATG	GAA									 T.e.i		 Met.	Leu	Ala	Thr	Ser	Ser
	Met	Glu	Ile	Ile	Ser	Leu	Lys	Arg	Pne	116	БСС			Leu	99			108
			63			72	mr.	uv-c	81 ACA	GAC	GAA	90 TCA	AGG	ATG	CCC	AAT	CTT	
	TTG	TTA	ACA	TCA	AAC	ATC								 Mot	Pro	 Asn	 Leu	Tyr
	Leu	Leu	Thr	Ser	Asn	Ile	Phe	Cys	Thr	Asp	GIU		ALG.	Met	1.50	•		162
			117			126		m»m	135	GAG	ССТ	144 AGA	GGA	GAT	153 CTA	GGC	TGG	
	AGC	AAA	AAG	TAA	TAT	GAC								7	 T.e.1	Glv	Trp	Glu
	Ser	Lys	Lys	Asn	Tyr	Asp	Lys	Tyr	Ser	Glu	Pro		GIĀ	Asp	nea	017		216
			171			180		C	189	GT'A	AAA	198 GAT	TGG	GCT	207 CCA	AAA	TTA	
	AAA	GAA	AGA	AGT	CTT	ACT	777	GAA								LVS	 Ile	Lys
	Lys	Glu	Arg	Ser	Leu	Thr	Phe	Glu	Glu	Val	Lys		пр	Ala	F10.	2,0		270
			225			234		222	243	CCA	CCT	252 TCT	GCA	GCC	261 AAC	CTG	CCA	
	ATG	TAA	AAA	CCT	GTA	GTC	AAC								 Asn	 Leu	 Pro	 Leu
	Met	Asn	Ŀys	Pro	Val	Val	Asn	Lys	Met	Pro	Pro		WIG	Ala	225	20,		324
			279			288	CD D	C N N	297	DD4	AGC	306 ACT	AGG	GCG	315 ATG	GCC	CAC	
	AGA	TTT	GGG	AGG	AAC	AIG	GAA						 Ara	ala	 Met	 Ala	 His	Leu
	Arg	Phe	Gly	Arg	Asn	Met	Glu	Glu	GIu	Arg	Ser	1111	, rag	Ala	2.00			378
			333			342	7 7 M	NGA.	351 GAG	GAC	AGC	360 CTC	TCC	AGA	369 TGG	GTC	CCA	
	CCT	CTG	AGA	CTC	GGA 						~ Cor	 T.e.1	 Ser	 Ara	Tro	 Val	Pro	Asn
	Pro	Leu	Arg	Leu	Gly	Lys	Asn	Arg	GIU	ASD	Ser			Arg	423			432
			387			396	3 C 3	ACA	405	ACA	GCC	414 AAA	AGC	ATT	ACC	AAG	ACC	
	CTG	CCC	CAG	AGG								 Lvc	 Ser	 Tle	 Thr	Lys	Thr	Leu
	Leu	Pro	Gln	Arg	Phe	Gly	Arg	Thr						Ile	477	-		486
			441			450	mcc.	אתעב	459	י יי תירא	CCA	468 TCT	ACC	TAA	477 GGG	CTA	CTC	
	AGT	AAT	TTG	CTC	CAG	CAG								7 cn	Glv		 Leu	Tyr
	Ser	Asn	Leu	Leu	Gln	Gln	Ser	Met	His	Ser	Pro	Ser	TILL	ASII	Gly	200		Tyr 540
			495			504			513		י אארי	522	ССТ	CAA	531 AAG	AAC	СТА	
	TCC	DTA	GCC	TGC	CAG	CCC	CAA	GAA	. A1C								 T 011	AGG
	 Ser	Met	Ala	. Cys	Glr	Pro	Gln	Glu	Ile	Gln	Asn	Pro	Gly	Gln	Lys	ASN	neu	Arg
												576			585			
	AGA	. cgc	545 GGA	, TTC	CAC	AAA	ATA	GAT	' GAT	GCA	GAA	TTG	AAA 	CAA	GAA	AAA	1777	,
		 -				 1 I.VS	Ile	Asp	Asp	Ala	Glu	Leu	Lys	Gln	Glu	Lys	* * *	
	Arg	Arc	1 617	/ FIIE	. 611	. 250		_	•									

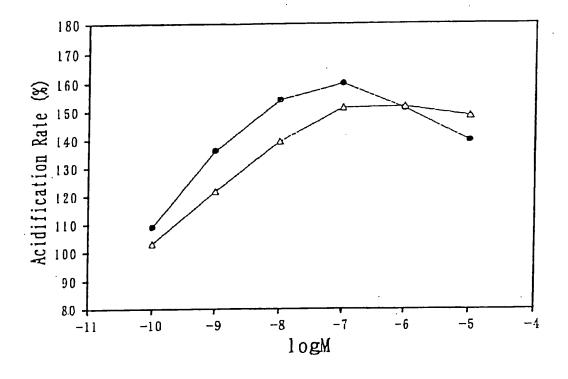
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	100	2.2.1	11	7	~~	mam	126		ጥአጥ	135		. care	144		איניע	153		ccc	162 GTA
	Ser	Lys	Gl	u G	ly	Tyr	Gly	Lys	Tyr	Tyr	Glr	Leu	Arg	Gly	Ile	Pro	Lys	Gly	Val
	አ አረግ	CNI	17		CT	CTC	180	بلملمك	CAA	189		. 222	198	TGG	ccc	207 GCA		AAA	216 GAT
	Lys	Glu	Ar	∄ S	er	Val	Thr	Phe	Gln	Glu	Leu	Lys	Asp	Trp	GIY				
	ATT	AAG	225 ATC		GT	CCA	234 GCC	CCT	GCC	243 AAC		. GTG	252 CCC	CAC	TCA	261 GCA			270 CTT
			·																
	116	Lys		-				710	Ala						Jer	315			324
	ccc	CTG	279 AG0	•			288 AGG	AAC			GAC	AGA		AGC	CCC				
	Pro	Leu	Arc	r Ph	 ne '	Glv	 Ara	 Asn			Asp			Ser	Pro	arg	Ala	Arg	Ala
			333				342			351			360			369			378
	AAC	ATG	GAG	GC	2A (GGG	ACC	ATG	AGC	CAT	TTT	CCC	AGC	CTG				TTT	GGG
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			387				396			405			414			423			432
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			441	-			 450			459			468			477			486
	CTG	CAC	TCC	CT		SCC '	TCC .		GAA	TCG		TAT	GCC	ATG	ACC	CGC		CAT	CAA
	Leu	 His	Ser	Le				 Ser				Tyr		Met				His	Gln
			495				504			513			522			531			540
	GAA .		CAG	AG		CT (GGT (GAG	CAA		AGG	AAA		GTG '	TTC		GAA .	ACA
	Glu							·	 -1,,	 Cln	Pro		 Tvc		·	Dhe	Thr	 Glu	 Thr
	GIU					210 (JIY (3111 (FIU			ÆΥ			1111		
	GAT	~ \ TI	549	C)	א א		558 558	ממר		567 444	מתמ		576 AAC	OTC (585 CA	GTC		594 CAA
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			603			6	512												
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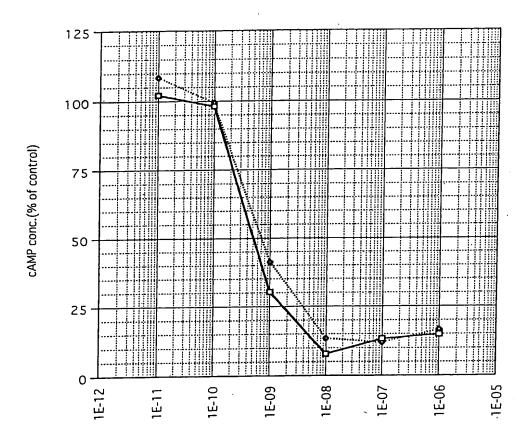
50	100	150	200	250
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MEIISSKIFI LLTLATSSLL TSNIFCADEL VMSNLHSKEN YDKYSEPRG- MEIISIKRFI LLMLATSSLL TSNIFCIDES RMPNLMSKKN YDKYSEPRGD MEIISSKRFI LLTLATSSFL TSNIFCIDES RMPNLMSKKN YDKYSEPRGD	60 70 80 90 100 YPKG-ER SINFEELKOW GPKNVIKWST PAVNKMPHSF ANL.PLRFGRN LGWEKER SLTFEEVKOW APRIKMYK PAVNKMPPSA ANL.PLRFGRN PKGVKER SVIFDELKOW GAKKUIKMSP APANKVPHSA ANL.PLRFGRN	VQEERSACAIT ANLPLRSTAN MENSIVRANP NLPORFGRITT TAKSVCRMLS MEEERSTRAM AFTLPLRICAN RETSLISAMVP NLPORFGRITT TAKSTITKTLS TEDRRSPRAR ANM	160 170 180 200 DICCISMHSP CANDIENSMT COHOELONPO DKOSRRLIER KIDDAELKOE NALCOSMHSP STNALLYSMA CORDEIONPG OKNIRRREPO KIDDAELKOE GIPOKSTHSL ASSESLYMMI ROHOELOSPG OFOFRKRNET ETDDAERKOE	X*
ннн	51	101	151	201
	51	101	151	201
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hLPLRF.aa	hLPLRF.aa	hLPLRF.aa	hLPLRF. aa	hLPLRF.aa
bLPLRF.aa	bLPLRF.aa	bLPLRF.aa	bLPLRF. aa	bLPLRF.aa
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1	TTTAGACTTAGACGAAATGGAAATTATTTCATTAAAACGATTCATTTTATTGACTGTG MetGlullelleSerLeuLysArgPhelleLeuLeuThrVal	14
1		118
59 15	GCAACTTCAAGCTTCTTAACATCAAACACCTTCTGTACAGATGAGTTCATGATGCCTCAT AlaThrSerSerPheLeuThrSerAsnThrPheCysThrAspGluPheMetMetProHis	34
13	ALGUME - COLOR DE COLOR DE LA ALGOGIA ALGORIA	178
119	TTTCACAGCAAAGAAGGTGACGGAAAATACTCCCAGCTGAGAGGAATCCCAAAAGGGGAA PheHisSerLysGluGlyAspGlyLysTyrSerGlnLeuArgGlyIleProLysGlyGlu	5 4
35	PHENISSOL A CANTESTA TO A CANTEST A CANTEST A A CANTEST A CANT	238
179	AAGGAAAGAAGTGTCAGTTTTCAAGAACTAAAAGATTGGGGGGCAAAGAATGTTATTAAG LysGluArgSerValSerPheGlnGluLeuLysAspTrpGlyAlaLysAsnVallleLys	74
55	LYSGIUAIGEELACACACACACACACACACACACACACACACACACACA	298
	ATGAGTCCAGCCCTGCCAACAAGTGCCCCACTCAGCAGCCAACCTGCCCCTGAGATTT	94
75	MetSerProAlaProAlaAshLySVd17101110111011101110111101111011110111	358
	GGAAGGACCATAGATGAGAAAAGAAGCCCCGCAGCACGGGTCAACATGGAGGCAGGGACC	114
95	GlyArgThrIleAspGluLySALgSellIonLaten	
	TOTAL CANCAGE CAGAGE CAGAGAGE CAGAGE CAGAGAGE CAGAGE CAGAGAGE CAGAGE CAGAGAGE CAGAGE CAGAGE CAGAGE CAGAGE CAGAGE CAGAGE CAGAGE CAGAGE CAGAGAG CAGAGE CAGAGE CAGAGE CAGAGE CAGAGE CAGAGE CAGAGE CAGAGE CAGAGAG CAGAGE CAGAGE CAGAGE CAGAGE CAGAGE CAGAGE CAGAGE CAGAGE CAGAGAG CAGAGE CAGAGE CAGAGE CAGAGE CAGAGE CAGAGE CAGAGE CAGAGE CAGAGAG CAGAGAG CAGAGAG CAGAGAG CAGAGAG CAGAGAG CAGAGAG CAGAGAG CAGAGAGAG	418
115	AGGAGCCATTTCCCCAGCCTGCCCCAAAGGTTTGGGAGAACAACAGCCAGAAGCCCCAAG ArgSerHisPheProSerLeuProGlnArgPheGlyArgThrThrAlaArgSerProLys	134
11-	THE STATE OF THE S	478
419	ACACCCGCTGATTTGCCACAGAAACCCCTGCACTCACTGGGCTCCAGCGAGTTGCTCTAC ThrProAlaAspLeuProGlnLysProLeuHisSerLeuGlySerSerGluLeuLeuTyr	154
13:	1 THEFT CALCALOG AGG AGG AGG AGG AGG AGG AGG AGG AGG A	538
479	GTCATGATCTGCCAGCACCAAGAAATTCAGAGTCCTGGTGGAAAGCGAACGAGGAGAGGA ValMetIleCysGlnHisGlnGluIleGlnSerProGlyGlyLysArgThrArgArgGly	174
15	5 Valmetliecysol	,598
•	9 GCGTTTGTGGAAACAGATGATGCAGAAAGGAAACCAGAAAAATAGGAAACCTCGAGCCCG	188
		100
17	5 Alarnevaldidining	618
59	9 ACTTCAAGAGGCTACGGAGC	188
18	8	

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F i g . 9



Conc.(M)